Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (currently amended) A method for identifying a differentially expressed protein in two different samples containing a population of proteins comprising:

a) providing two equal protein pools from a reference sample and two equal protein pools from an experimental sample;

b) labeling the protein pools with a substantially chemically identical isotopically different protein labeling reagent for proteins, wherein one pool from each of the reference and experimental pools is labeled with an isotopically heavy protein labeling reagent to provide an isotopically heavy-labeled reference pool and an isotopically heavy-labeled experimental pool, and wherein the remaining reference and experimental pools are labeled with an isotopically light protein labeling reagent to provide an isotopically light-labeled reference pool and an isotopically light-labeled experimental pool;

c) combining the isotopically light-labeled reference pool with the isotopically heavy-labeled experimental pool to provide a first protein mixture;

d) combining the isotopically heavy-labeled reference pool with the isotopically light-labeled experimental pool to provide a second protein mixture;

e) detecting the labeled proteins from each of the two mixtures; and

f) comparing the labeling pattern obtained for the labeled proteins in the first mixture with the labeling pattern obtained for the labeled proteins in the ~~and~~ second mixture, wherein ~~an inverse labeling pattern~~ a qualitative mass shift or an isotope peak intensity ratio reversal between the two labeling patterns is indicative of a ~~of a protein in the second mixture compared with the labeling pattern of the protein in the first mixture is indicative of the~~ differentially expressed protein in the two different samples.

2. (original) The method of claim 1, which further comprises enzymatically or chemically cleaving the labeled proteins in the first and second mixtures to provide peptide mixtures prior to step (e).

3. (original) The method of claim 2, which further comprises sequencing one of the peptides to identify the differentially expressed protein from which the peptide originated.

4. (original) The method of claim 3, wherein sequencing of the peptide is performed utilizing tandem mass spectrometry or post source decay (PSD).

5. (original) The method of claim 1, which further comprises sequencing the differentially expressed protein to identify the protein.

6. (original) The method of claim 5, wherein sequencing of the differentially expressed protein is performed utilizing tandem mass spectrometry or PSD.

7. (original) The method of claim 1, which further comprises separating the labeled proteins from each of the first and second mixtures prior to step (e).

8. (original) The method of claim 7, wherein the step of separating the labeled proteins from the two mixtures is carried out using a technique selected from the group consisting of ammonium sulfate precipitation, isoelectric focusing, size exclusion chromatography, ion exchange chromatography, adsorption chromatography, reverse phase chromatography, affinity chromatography, ultrafiltration, immunoprecipitation and combinations thereof.

9. (original) The method of claim 2, which further comprises separating the labeled peptides from each of the first and second mixtures prior to step (e).

10. (original) The method of claim 9, wherein the step of separating the labeled peptides from the two mixtures is carried out using a technique selected from the group consisting of size exclusion chromatography, ion exchange chromatography, adsorption chromatography, reverse phase chromatography, affinity chromatography, immunoprecipitation and combinations thereof.

11. (original) The method of claim 1, wherein the labeled proteins are detected by mass spectrometry.

12. (original) The method of claim 2, wherein the labeled peptides are detected by mass spectrometry.

13. (original) The method of claim 1, which further comprises subjecting the samples to at least one fractionation technique to reduce the complexity of proteins in the samples prior to step (a).

14. (original) The method of claim 2, which further comprises subjecting the isotopically labeled proteins of the first and second mixtures to at least one fractionation technique to reduce

the complexity of proteins in the first and second mixtures prior to cleaving the labeled proteins in the first and second mixtures.

15. (original) The method of claim 13, wherein the fractionation technique is selected from the group consisting of ammonium sulfate precipitation, isoelectric focusing, size exclusion chromatography, ion exchange chromatography, adsorption chromatography, reverse phase chromatography, affinity chromatography, ultrafiltration, immunoprecipitation and combinations thereof.

16. (original) The method of claim 1, wherein the two samples differ in cell type, tissue type, physiological state, disease state, developmental stage, environmental conditions, nutritional conditions, chemical stimuli or physical stimuli.

17. (previously amended) The method of claim 1, wherein the isotopically heavy protein labeling reagent contains a stable heavy isotope selected from the group consisting of ^{2}H, ^{13}C, ^{15}N, ^{17}O, ^{18}O and ^{34}S.

18. (original) The method of claim 1, wherein the isotopically light protein labeling reagent contains a stable light isotope selected from the group consisting of H, ^{12}C, ^{14}N, ^{16}O and ^{32}S.

19. (original) The method of claim 1, wherein the isotopically heavy protein labeling reagent contains ^{18}O and the isotopically light protein labeling reagent contains ^{16}O.

20. (original) The method of claim 1, wherein the protein labeling reagent contains an affinity tag.

21. (original) The method of claim 1, wherein the samples are selected from the group consisting of cell homogenates, cell fractions, tissue homogenates, biological fluids, tears, feces, saliva and lavage fluids.

22. (original) The method of claim 1, wherein the differentially expressed protein is selected from the group consisting of cell surface proteins, membrane proteins, cytosolic proteins and organelle proteins.

23. (currently amended) A method for identifying a differentially expressed protein in two different samples containing a population of proteins comprising:

a) providing two equal protein pools from a reference sample and two equal protein pools from an experimental sample;

b) proteolyzing each protein pool in the presence of isotopically labeled water, wherein one pool from each of the reference and experimental pools is labeled with ^{18}O-water to provide an ^{18}O-labeled reference pool and an ^{18}O-labeled experimental pool, and wherein the remaining reference and experimental pools are labeled with ^{16}O-water to provide an ^{16}O-labeled reference pool and an ^{16}O-labeled experimental pool;

c) combining the ^{16}O-labeled reference pool with the ^{18}O-labeled experimental pool to provide a first mixture containing ^{16}O- and ^{18}O-labeled peptides;

d) combining the ^{18}O labeled reference pool with the ^{16}O-labeled experimental pool to provide a second mixture containing ^{18}O- and ^{16}O-labeled peptides;

e) detecting the labeled peptides from each of the two mixtures; and

f) comparing the labeling pattern obtained for the labeled proteins in the first mixture with the labeling pattern obtained for the labeled proteins in the ~~and~~ second mixture, wherein ~~an inverse labeling pattern~~ a qualitative mass shift or an isotope peak intensity ratio reversal between the two labeling patterns is indicative of a ~~of a protein in the second mixture compared with the labeling pattern of the protein in the first mixture is indicative of the~~ differentially expressed protein in the two different samples.

24. (original) The method of claim 23, which further comprises separating the labeled peptides in the two mixtures prior to step (e).

25. (original) The method of claim 24, wherein the step of separating the labeled peptides in the two mixtures is carried out using a technique selected from the group consisting of size exclusion chromatography, ion exchange chromatography, adsorption chromatography, reverse phase chromatography, affinity chromatography, immunoprecipitation and combinations thereof.

26. (original) The method of claim 23, wherein detection of the labeled peptides is carried out by mass spectrometry.

27. (original) The method of claim 23, which further comprises sequencing one of the peptides to identify the differentially expressed protein from which the peptide originated.

28. (original) The method of claim 27, wherein sequencing of the peptide is performed utilizing tandem mass spectrometry or PSD.

29. (original) The method of claim 23, which further comprises subjecting the samples to at least one fractionation technique to reduce the complexity of proteins in the samples prior to step a).

30. (original) The method of claim 23, which further comprises subjecting the labeled peptides of the first and second mixtures to at least one fractionation technique to separate undesirable peptides from the first and second mixtures prior to step (e).

31. (original) The method of claim 29, wherein the fractionation technique is selected from the group consisting of ammonium sulfate precipitation, isoelectric focusing, size exclusion chromatography, ion exchange chromatography, adsorption chromatography, reverse phase chromatography, affinity chromatography, ultrafiltration, immunoprecipitation and combinations thereof.

32. (original) The method of claim 23, wherein the samples are selected from the group consisting of cell homogenates, cell fractions, tissue homogenates, biological fluids, tears, feces, saliva and lavage fluids.

33. (original) The method of claim 23, wherein the differentially expressed protein is selected from the group consisting of cell surface proteins, membrane proteins, cytosolic proteins and organelle proteins.

34. (original) The method of claim 23, wherein the two samples differ in cell type, tissue type, physiological state, disease state, developmental stage, physiological state, environmental conditions, nutritional conditions, chemical stimuli or physical stimuli.

35. (currently amended) A method for identifying a differentially expressed protein in two different samples containing a population of proteins comprising:

a) providing two equal protein pools from a reference sample and two equal protein pools from an experimental sample;

b) proteolyzing the proteins in each of the protein pools to provide peptide pools;

c) labeling each peptide pool with isotopically labeled water, wherein one peptide pool from each of the reference and experimental pools is labeled with ^{18}O-water to provide an ^{18}O-labeled reference peptide pool and an ^{18}O-labeled experimental peptide pool, and wherein the remaining reference and experimental peptide pools are labeled with ^{16}O-water to provide an ^{16}O labeled reference peptide pool and an ^{16}O-labeled experimental peptide pool;

d) combining the ^{16}O-labeled reference pool with the ^{18}O-labeled experimental pool to provide a first mixture containing ^{16}O- and ^{18}O-labeled peptides;

e) combining the ^{18}O-labeled reference pool with the ^{16}O-labeled experimental pool to provide a second mixture containing ^{18}O- and ^{16}O-labeled peptides;

f) detecting the labeled peptides from each of the two mixtures; and

g) comparing the labeling pattern obtained for the labeled proteins in the first mixture with the labeling pattern obtained for the labeled proteins in the ~~and~~ second mixture, wherein ~~an inverse labeling pattern~~ a qualitative mass shift or an isotope peak intensity ratio reversal between the two labeling patterns is indicative of a ~~of a protein in the second mixture compared with the labeling pattern of the protein in the first mixture is indicative of the~~ differentially expressed protein in the two different samples.

36. (original) The method of claim 35, which further comprises separating the labeled peptides from the first and second mixtures prior to step (f).

37. (original) The method of claim 36, wherein the step of separating the labeled peptides from the two mixtures is carried out using a technique selected from the group consisting of size exclusion chromatography, ion exchange chromatography, adsorption chromatography, reverse phase chromatography, affinity chromatography, immunoprecipitation and combinations thereof.

38. (original) The method of claim 35, wherein detection of the labeled peptides is carried out by mass spectrometry.

39. (original) The method of claim 35, which further comprises sequencing one of the peptides to identify the differentially expressed protein from which the peptide originated.

40. (original) The method of claim 39, wherein sequencing of the peptide is performed utilizing tandem mass spectrometry or PSD.

41. (original) The method of claim 35, which further comprises subjecting the samples to at least one fractionation technique to reduce the complexity of proteins in the samples prior to step (a).

42. (original) The method of claim 35, which further comprises subjecting the labeled peptides of the first and second mixtures to at least one fractionation technique to separate undesirable peptides from the first and second mixtures prior to step (e).

43. (original) The method of claim 41, wherein the fractionation technique is selected from the group consisting of ammonium sulfate precipitation, isoelectric focusing, size exclusion chromatography, ion exchange chromatography, adsorption chromatography, reverse phase liquid chromatography, affinity chromatography, ultrafiltration, immunoprecipitation and combinations thereof.

44. (original) The method of claim 35, wherein the samples are selected from the group consisting of cell homogenates, cell fractions, tissue homogenates, biological fluids, tears, feces, saliva and lavage fluids.

45. (original) The method of claim 35, wherein the differentially expressed protein is selected from the group consisting of cell surface proteins, membrane proteins, cytosolic proteins and organelle proteins.

46. (original) The method of claim 35, wherein the two samples differ in cell type, tissue type, physiological state, disease state, developmental stage, physiological state, environmental conditions, nutritional conditions, chemical stimuli or physical stimuli.

47. (currently amended) A method for identifying a differentially expressed protein in two different samples containing a population of proteins comprising:

a) providing two equal protein pools from a reference sample and two equal protein pools from an experimental sample wherein one pool from each of the reference and experimental pools is produced by cultivation in a medium containing an isotopically heavy-labeled assimilable source to provide an isotopically heavy-labeled reference pool and an isotopically heavy-labeled experimental pool, and wherein the remaining reference and experimental pools are produced by cultivation in a medium containing an isotopically light-labeled assimilable source to provide an isotopically light-labeled reference pool and an isotopically light-labeled experimental pool;

b) combining the isotopically light-labeled reference pool with the isotopically heavy-labeled experimental pool to provide a first protein mixture;

c) combining the isotopically heavy-labeled reference pool with the isotopically light-labeled experimental pool to provide a second protein mixture;

d) detecting the labeled proteins from each of the two mixtures; and

e) comparing the labeling pattern obtained for the labeled proteins in the first mixture with the labeling pattern obtained for the labeled proteins in the ~~and~~ second mixture, wherein ~~an inverse labeling pattern~~ a qualitative mass shift or an isotope peak intensity ratio reversal between the two labeling patterns is indicative of a ~~of a protein in the second mixture compared with the labeling pattern of the protein in the first mixture is indicative of the~~ differentially expressed protein in the two different samples.

48. (original) The method of claim 47, which further comprises enzymatically or chemically cleaving the labeled proteins in the first and second mixtures to provide peptide mixtures prior to step (d).

49. (original) The method of claim 47, wherein the assimilable source is selected from the group consisting of ammonium salts, glucose, water and amino acids.

50. (new) The method of claim 1, in which the detection of labeled proteins from each of the two mixtures and subsequent comparison of their labeling patterns is not performed by quantitatively calculating the ratio of isotopically light to isotopically heavy signals of a protein.

51. (new) The method of claim 23, in which the detection of labeled proteins from each of the two mixtures and subsequent comparison of their labeling patterns is not performed by quantitatively calculating the ratio of isotopically light to isotopically heavy signals of a protein.

52. (new) The method of claim 35, in which the detection of labeled proteins from each of the two mixtures and subsequent comparison of their labeling patterns is not performed by quantitatively calculating the ratio of isotopically light to isotopically heavy signals of a protein.

53. (new) The method of claim 47, in which the detection of labeled proteins from each of the two mixtures and subsequent comparison of their labeling patterns is not performed by quantitatively calculating the ratio of isotopically light to isotopically heavy signals of a protein.